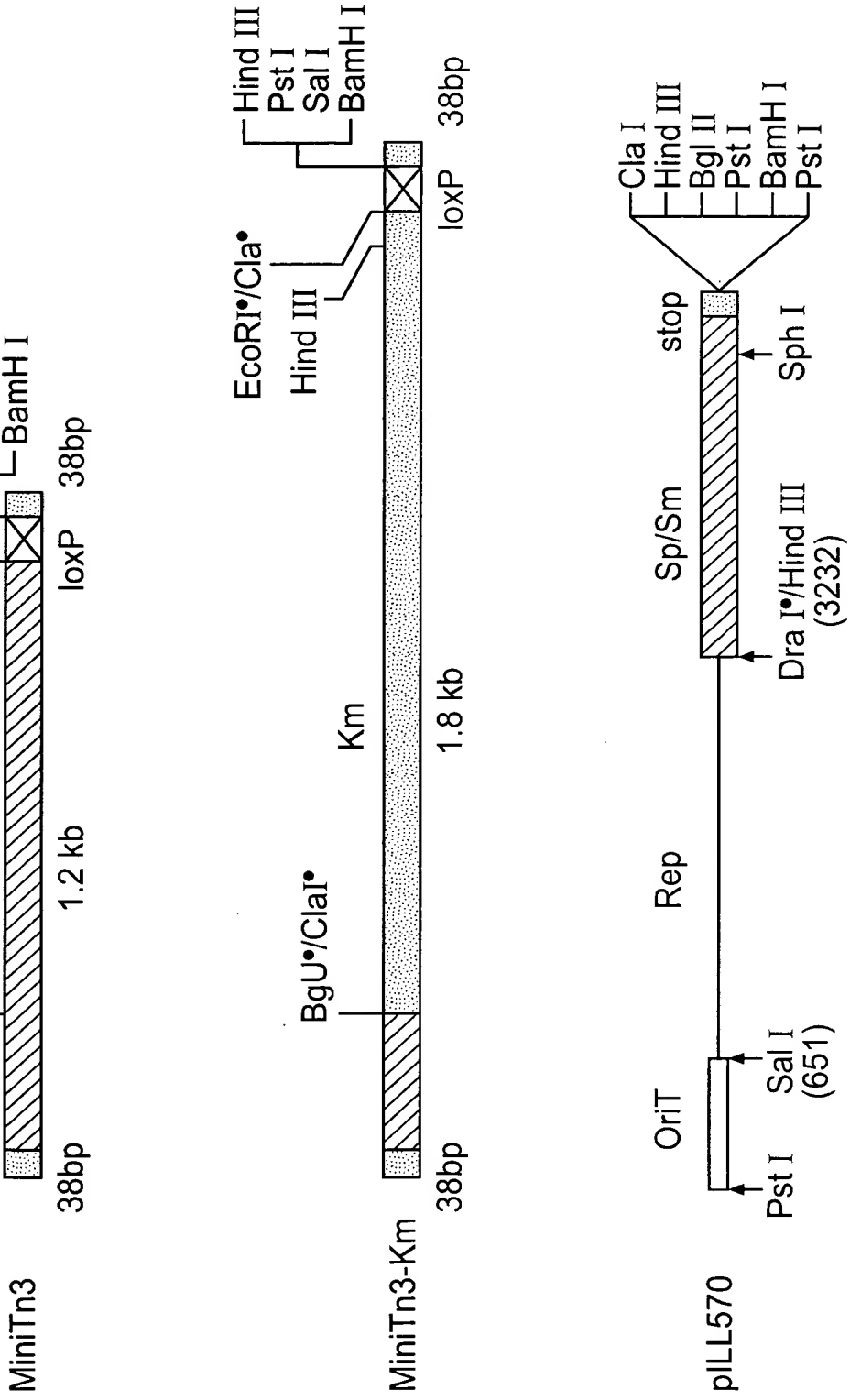


FIG. 1A

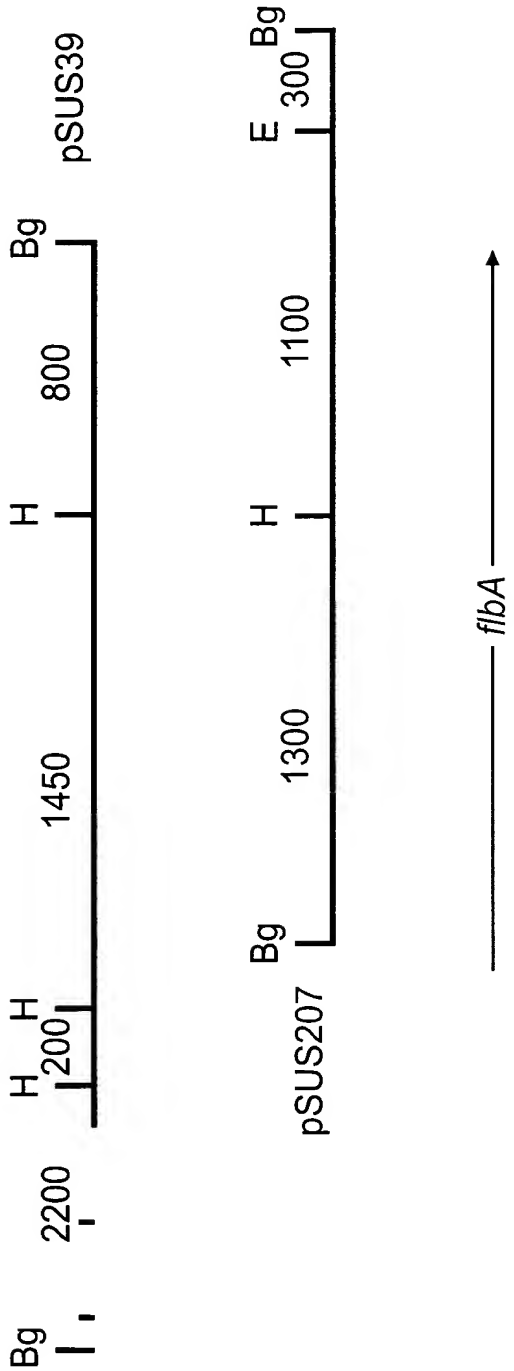


FIG. 1B

```
1                                                   31
AGC TTT TTT GTG CCA TAC TTT TAA ACT TTA TAT TAT AAT AAG AGA CAA ACA CAC CTA CCA

61                                                  91
AAA TTA AGG CAT TGA TTT TAG ATT ATG GCA AAC GAA CGC TCC AAA TTA GCT TTT AAA AAG
                                    M   A   N   E   R   S   K   L   A   F   K   K
121                                                 151
ACT TTC CCT GTC TTT AAA CGC TTC TTG CAA TCC AAA GAC TTA GCC CTT GTG GTC TTT GTG
T   F   P   V   F   K   R   F   L   Q   S   K   D   L   A   L   V   V   F   V
181                                                 211
ATA GCG ATT TTA GCG ATC ATT ATC GTG CCG TTA CCG CCT TTT GTG TTG GAT TTT TTA CTC
I   A   I   L   A   I   I   I   V   P   L   P   P   F   V   L   D   F   L   L
241                                                 271
ACG ATT TCT ATC GCG CTA TCG GTG TTG ATT ATT TTA ATC GGG CTT TAT ATT GAC AAA CCG
T   I   S   I   A   L   S   V   L   I   I   L   I   G   L   Y   I   D   K   P
301                                                 331
ACT GAT TTT AGC GCT TTC CCC ACT TTA TTA CTC ATT GTA ACC TTA TAC CGC TTG GCT TTA
T   D   F   S   A   F   P   T   L   L   L   I   V   T   L   Y   R   L   A   L
361                                                 391
AAT GTC GCC ACC ACT AGA ATG ATT TTA ACC CAA GGC TAT AAA GGG CCT AGC GCG GTG AGC
N   V   A   T   T   R   M   I   L   T   Q   G   Y   K   G   P   S   A   V   S
421                                                 451
ATT ATT ATC ACG GCG TTT GGG GAA TTT AGC GTG AGC GGG AAT TAT GTG ATT GGG GCT ATT
I   I   I   T   A   F   G   E   F   S   V   S   G   N   Y   V   I   G   A   I
```

FIG. 2A

```
481                                                 511
ATC TTT AGT ATT TTA GTG CTG GTG AAT TTA TTA GTG GTT ACT AAT GGT TCT ACT AGG GTT
I   F   S   I   L   V   L   V   N   L   L   V   V   T   N   G   S   T   R   V
541                                                 571
ACT GAA GTT AGG GCG CGA TTT GCC CTA GAC GCT ATG CCA GGA AAG CAA ATG GCG ATT GAT
T   E   V   R   A   R   F   A   L   D   A   M   P   G   K   Q   M   A   I   D
601                                                 631
GCG GAT TTA AAT TCA GGG CTT ATT GAT GAT AAG GAA GCT AAA AAA CGG CGC GCC GCT CTA
A   D   L   N   S   G   L   I   D   D   K   E   A   K   K   R   R   A   A   L
661                                                 691
AGC CAA GAA GCG GAT TTT TAT GGT GCG ATG GAT GGC GCG TCT AAA TTT GTC AAA GGC GAT
S   Q   E   A   D   F   Y   G   A   M   D   G   A   S   K   F   V   K   G   D
721                                                 751
GCG ATC GCT TCT ATC ATT ATC ACG CTT ATC AAT ATC ATT GGG GGT TTT TTA GTG GGC GTG
A   I   A   S   I   I   I   T   L   I   N   I   I   G   G   F   L   V   G   V
781                                                 811
TTC CAA AGG GAT ATG AGC TTG AGC TTT AGT GCT AGC ACT TTC ACT ATC TTA ACC ATT GGC
F   Q   R   D   M   S   L   S   F   S   A   S   T   F   T   I   L   T   I   G
841                                                 871
GAT GGG CTT GTA GGG CAA ATC CCT GCC TTA ATC ATT GCG ACA CGG ACC GGT ATT GTC GCC
D   G   L   V   G   Q   I   P   A   L   I   I   A   T   R   T   G   I   V   A
901                                                 931
ACT CGC ACC ACG CAA AAC GAA GAA GAG GAC TTT GCT TCT AAG CTC ATC ACA CAG CTC ACC
T   R   T   T   Q   N   E   E   E   D   F   A   S   K   L   I   T   Q   L   T
```

Replacement Sheet

FIG. 2B

```
961                                                 991
AAT AAA AGC AAA ACT TTA GTG ATT GTG GGG GCG ATT TAT TGC TTT TGC ACC ATT CCT GGA
N   K   S   K   T   L   V   I   V   G   A   I   Y   C   F   C   T   I   P   G
1021                                                1051
CTC CCT ACC TTT TCT TTA GCG TTT GTA GGG GCT CTC TTT TTA TTC ATC GCA TGG CTG ATT
L   P   T   F   S   L   A   F   V   G   A   L   F   L   F   I   A   W   L   I
1081                                                1111
AGC AGG GAG GGA AAG GAC GGG TTG CTC ACT AAA TTA GAA AAT TAT TTG AGT CAA AAA TTC
S   R   E   G   K   D   G   L   L   T   K   L   E   N   Y   L   S   Q   K   F
1141                                                1171
GGC TTG GAT TTG AGC GAA AAA CCC CAC AGC TCC AAA ATC AAA CCC CAC GCC CCC ACC ACA
G   L   D   L   S   E   K   P   H   S   S   K   I   K   P   H   A   P   T   T
1201                                                1231
AGG GCT AAA ACC CAA GAA GAG ATT AAA AGA GAA GAA GAG CAA GCC ATT GAT GAA GTG TTA
R   A   K   T   Q   E   E   I   K   R   E   E   E   Q   A   I   D   E   V   L
1261                                                1291
AAA ATT GAA TTT TTA GAA TTG GCT TTA GGC TAT CAG CTC TAC AGC TTA GCG GAC ATG AAA
K   I   E   F   L   E   L   A   L   G   Y   Q   L   Y   S   L   A   D   M   K
1321                                                1351
CAA GGG GGC GAT TTG TTA GAA AGG ATT AGG GGT ATT AGA AAA AAG ATA GCG AGC GAT TAT
Q   G   G   D   L   L   E   R   I   R   G   I   R   K   K   I   A   S   D   Y
1381                                                1411
GGT TTT TTG ATG CCT CAA ATT AGG ATT AGG GAT AAT TTA CAA CTC CCC CCA ACG CAT TAT
G   F   L   M   P   Q   I   R   I   R   D   N   L   Q   L   P   P   T   H   Y
```

FIG. 2C

```
1441                                                1471
GAA ATC AAG CTT AAG GGC ATT GTG ATT GGT GAA GGC ATG GTG ATG CCG GAT AAG TTT TTA
E   I   K   L   K   G   I   V   I   G   E   G   M   V   M   P   Q   K   F   L
1501                                                1531
GCC ATG AAT ACC GGT TTT GTG AAT AAA GAA ATT GAA GGC ATT CCT ACT AAA GAG CCG GCT
A   M   N   T   G   F   V   N   K   E   I   E   G   I   P   T   K   E   P   A
1561                                                1591
TTT GGA ATG GAC GCT TTA TGG ATT GAA ACT AAA AAT AAA GAA GAA GCC ATC ATT CAA GGC
F   G   M   D   A   L   W   I   E   T   K   N   K   E   E   A   I   I   Q   G
1621                                                1651
TAT ACC ATT ATT GAT CCA AGC ACC GTT ATT GCG ACG CAC ACC AGC GAA TTA GTG AAA AAA
Y   T   I   I   D   P   S   T   V   I   A   T   H   T   S   E   L   V   K   K
1681                                                1711
TAC GCT GAA GAT TTT ATC ACT AAA GAT GAA GTG AAA TCC CTT TTA GAG CGC TTG GCC AAA
Y   A   E   D   F   I   T   K   D   E   V   K   S   L   L   E   R   L   A   K
1741/581                                            1771
GAC TAT CCT ACG ATT GTA GAA GAG AGT AAA AAA ATC CCC ACC GGT GCG ATC CGA TCA GTC
D   Y   P   T   I   V   E   E   S   K   K   I   P   T   G   A   I   R   S   V
1801                                                1831
TTG CAA GCC TTG TTG CAT GAA AAA ATC CCC ATT AAA GAC ATG CTC ACT ATT TTA GAA ACG
L   Q   A   L   L   H   E   K   I   P   I   K   D   M   L   T   I   L   E   T
1861                                                1891
ATT ACC GAT ATT GCG CCA TTA GTT CAA AAC GAT GTG AAT ATC TTA ACC GAA CAA GTG AGG
I   T   D   I   A   P   L   V   Q   N   D   V   N   I   L   T   E   Q   V   R
```

FIG. 2D

```
1921                                                1951
GCG AGG CTT TCT AGG GTG ATC ACT AAC GCT TTT AAA TCT GAA GAC GGG CGT TTG AAA TTT
A   R   L   S   R   V   I   T   N   A   F   K   S   E   D   G   R   L   K   F
1981                                                2011
TTA ACC TTT TCT ACC GAT AGC GAA CAA TTT TTG CTT AAT AAA TTG CGA GAA AAT GGC ACT
L   T   F   S   T   D   S   E   Q   F   L   L   N   K   L   R   E   N   G   T
2041                                                2071
TCT AAG AGC CTA CTA CTC AAT GTG GGC GAA TTG CAA AAA CTC ATT GAA GCG GTC TCT GAA
S   K   S   L   L   L   N   V   G   E   L   Q   K   L   I   E   A   V   S   E
2101                                                2131
GAG GCC ATG AAA GTC TTG CAA AAA GGG ATC GCT CCG GTG ATT TTG ATC GTA GAG CCT AAT
E   A   M   K   V   L   Q   K   G   I   A   P   V   I   L   I   V   E   P   N
2161                                                2191
TTA AGA AAA GCC CTT TCT AAT CAA ATG GAG CAG GCT AGG ATT GAT GTA ATC GTG CTA AGC
L   R   K   A   L   S   N   Q   M   E   Q   A   R   I   D   V   I   V   L   S
2221                                                2251
CAT GCT GAA TTA GAT CCT AAC TCT AAT TTT GAA GCC TTA GGC ACG ATC CAT ATT AAC TTT
H   A   E   L   D   P   N   S   N   F   E   A   L   G   T   I   H   I   N   F
2281                                                2311
TAA GGG ATA AAT AAT TGA TAA AAA AGG AGA ATG ATG CAA GTT TAT CAC CTT TCA CAC ATT

2341                                                2371
GAT TTA GAC GGC TAT GCA TGC CAG CTT GTT TCA AAA CAA TTT TTT AAA AAT ATC CAA TGC

2401                                                2431
TAT AAC GCT AAT TAC GGG CGT GAA GTC TCA GCG AGA ATT TAT GAG ATT TTA AAC GCG ATC

2461                                                2491
GCT CAA TCT AAA GAG AGT GAA TTC CTT ATT TTG ATT AGC GA
```

FIG. 2E

```
  1 MANKRS-KLAFKKTFPVFKRFLQSKDLALVVFVIAILAIIIVPLPPFVLDFLLTISIALS HpF1bA
  1 MAKNKIVDLVFPFLGPLIAPVLKAKSLTIVGFLVCILAIIIVPLPSPILDFFLALSIALS CjF1bA
  1 MADAAAPNASSMPSAKSLLDGLMRGEMGLALGVVGIIVLLIIPVPAPLLDVLLAISLTGS CcF1bF
  1 ---------MNPHDLEWLNRIGERKDIMLAVLLLAVVFMMVLPLPPLVLDILIAVNMTIS YpLcrD
  1 ------------MLLSLLNSARLRPRLLILVLMVMIISMFVIPLPTYLVDFLIALNIVLA StInvA
  1 --------------------------------MVMIIAMLIIPLPTYLVDFLIGLNIVLA SfMxiA
                                       . .    . *.*   .*.. .  . ..

 60 VLIILIGLYIDKPTDFSAFPTLLLIVTLYRLALNVATTRMILTQGYKGPSAVSIIITAFG HpF1bA
 61 VLIILISIYIPKPTDLTTFPTLILIITLFRLSLNIATTRMILSEGQNGPEAVSEIIAAFG CjF1bA
 61 VLILMTAILIKKPLEFTSFPTVLLVTTLFRLGLNIASTRLILSHGQEGTGGAGAVIEAFG CcF1bF
 52 VVLLMIAIYINSPLQFSAFPAVLLVTTLFRLALSVSTTRMILLQ-----ADAGQIVYTFG YpLcrD
 49 ILVFMGSFYIDRILSFSTFPAVLLITTLFRLALSISTSRLILIEA-----DAGEIIATFG StInvA
 29 ILVFMGSFYIERILSFSTFPSVLLITTLFRLALSISTSRLILVDADRGK-----IITTFG SfMxiA
    ..      .*  .. .. ** ..*..**.** * . ..* **             ..  **

120 EFSVSGNYVIGAIIFSILVLVNLLVVTNGSTRVTEVRARFALDAMPGKQMAIDADLNSGL HpF1bA
121 EFVVGGNMVIGVIVFCILVLINFMVVTKGSTRVSEVQARFTLDAMPGKQMAIDADLNAGL CjF1bA
121 HLMMQGNFVIGVIVFIILIVVNFMVVTKGSGRIAEVAARFTLDSMPGKQMAIDADLSTGL CcF1bF
107 NFVVGGNLIVGIVIFLIITIVQFLVITKGSERVAEVSARFSLDAMPGKOMSIDGDMRAGV YpLcrD
104 QFVIGDSLAVGFVVFSIVTVVQFIVITKGSERVAEVAARFSLDGMPGKQMSIDADLKAGI StInvA
 84 QFVIGDSLAVGFVIFSIVTVVQFIVITKGSERVAEVAARFSLDGMPGKQMSIDADLKAGI SfMxiA
     .. ..    *   * *   . . * *.** *..** *** ** ****** **.*. .*.
```

Replacement Sheet

FIG. 3A

```
180 IDDKEAKKRRAALSQEADFYGAMDGASKFVKGDAIASIIITLINIIGGFLVGVFQRDMSL HpF1bA
181 IDEQTARARRQEVIAEANFYGAMDGSSKFIKGDAVAGIIITIINIIGGFLIGSFQHDMAL CjF1bA
181 ISQDEAKIRRKELEQESTFFGAMDGASKFVKGDAIAGLIITAINIIGGIIIGVVQHKMPF CcF1bF
167 IDVNEARERRATIEKESQMFGSMDGAMKFVKGDAIAGLIIIFVNILGGVTIGVTQKGLAA YpLcrD
164 IDADAARERRSVLERESQLYGSFDGAMKFIKGDAIAGIIIIFVNFIGGISVGMTRHGMDL StInvA
144 IDAAGAKERRSILERESQLYGSFDGAMKFIKGDAIAGIIIIFVNLIGGISVGMSQHGMSL SfMxiA
    *.   *  **  .. *.  .*  ** **  ****.*..**   *..**   *  .. . .

240 SFSASTFTILTIGDGLVGQIPALIIATRTGIVATRTTQNEEEDFASKLITQLTNKSKTLV HpF1bA
241 SDAASTYTILTIGDGLVSQIPGLITSTATAIIITRASKDEENFAEGTLTQLLSEYRTLLI CjF1bA
241 GDAASTYTIMTIGDGLVSQIPALIISIAAGMVVSKAGVEGSADKALTTQLAMNPVGLGMV CcF1bF
227 AEALQLYSILTVGDGMVSQVPALLIAITAGIIVTRVSSEDSSDLGSDIGKQVVAQPKAML YpLcrD
224 SSALSTYTMLTIGDGLVAQIPALLIAISAGFIVTRVNGDTDN-MGRNIMTQLLNNPFVLV StInvA
204 SGALSTYTILTIGDGLVSQIPALLISISAGFMLTRVNGDSDN-MGRNIMSQIFGNPFVLI SfMxiA
    . . ......*.***.*.*.*.* . . ..   ..              .       .

300 IVGAIYC-FCTIPGLPTFSLAFVGALFLFIAWLISREGKDGLLTKLENYLSQKFGLDLSE HpF1bA
301 VGFVLFI-FALVPGLPTLSLGFMALVFLSLGYLTKQVKEGKI-----DITTVKKSKPSAA CjF1bA
301 SASSG-I-IALIPGMPIFPFAAMALA----------------------------AGALAY CcF1bF
287 IGGVLLLLFGLIPGFPTVTFLILALLVGCGGYMLSRKQSRNDEANQDLQSILTSGSGAPA YpLcrD
283 VTAILTISMGTLPGFPLPVFVILSVVLSVLFYFKFREAKRSAAKPKTSKGEQPLSIEEKE StInvA
263 VTSALALAIGMLPGFPFFVFFLIAVTLTALFYYKKVVEKEKSLSESDSSGYTG------- SfMxiA
        .       ** *   .   .       .
```

Replacement Sheet

FIG. 3B

```
359 KPHSSKIKPHAPTTRAKTQEEIKREEEQAIDEVLKIEFLELALGYQLYSLADMKQGGDLL HpFlbA
355 VASQSGAGGTTAAPAKKSEEEILKEEEHKINDILKVEILELELGYGLIKLAE----NELT CjFlbA
331 KRVQDAKKPKALDPADLEAAAPSEPEEEPISASLAIDDVKIELGYGLLTLINDLDGRKLT CcFlbF
347 ARTKAKTSGANKGRLGEQEAFAMTVPLLIDVDS--------------SQQEALEANALN YpLcrD
343 GSSLGLIGDLDKVSTE------------------------TVPLILLVPKSRREDLEKA StInvA
316 ----------------TFDIDNTHDSSLAMIENLDRISSETVPLILLFAENKINANDME SfMxiA
                                    *          *          *

419 ERIRGIRKKIASDYGFLMPQIRIRDNLQLPPTHYEIKLKGIVIGPGMVMPDKFLAMNTGF HpFlbA
411 ERIRSMRRSIAESLGFLMPKIRIRDNLRLKPNEYSFKLKGVSIASAEIYPDKYLAMDSGF CjFlbA
391 DQIRALRKTLASEYGFVMPPVRILDNMRLANQGYAIRIKEMEAGAGEVRLGCLMCMDPRG CcFlbF
392 DELVRVRRALYLDLGVPFPGIHLRFNEGMGEGEYIISLQEVPVARGELKAGYLLVRESVS YpLcrD
378 QLAERLRSQFFIDYGVRLPEVLLRDGEGLDDNSIVLLINEIRVEQFTVYFD--LMRVVNY StInvA
359 GLIERIRSQFFIDYGVRLPTILYRTSNELKVDDIVLLINEVRADSFNIYFDKVCITDENG SfMxiA
      .   *     ..*   * .  ...  .    .    .          .  .

479 VNKEIEGIPTKEPAF--GMDALWIETKNKEEAIIQGYTIIDPSTVIATHTSELVKKYAED HpFlbA
471 ITEEIEGIATKEPAF--NSDALWIDANLKDEATLNGYIVIDPASVISTHMSELIKAHASE CjFlbA
451 GOVELPGEHVREPAF--GLPATWIADDLREEATFRGYTVVDPATVLTTHLTEILKENMAD CcFlbF
452 QLELLGIPYEKGEHLLPDQEAFWVSVEYEERLEKSQLEFFSHSQVLTWHLSHVLREYAED YpLcrD
436 SDEVVSFGINPTIHQQGSSQYFWVTHEEGEKLRELGYVLRNALDELYHCLAVTVARNVNE StInvA
419 DIDALGIPVVSTS--YNERVISWVDVSYTENLTNIDAKIKSAQDEFYHQLSQALLNNINE SfMxiA
                       . *      .     ..       .   ...
```

Replacement Sheet

FIG. 3C

```
537 FITKDEVKSLLERLAKDYPTIVEESK-KI-PTGAIRSVLQALLHEKIPIKDMLTILETIT  HpFlbA
529 LLTRQEVQNLLDKVKNDYPIIVEGAL-GVAPVSLIQKILKDLLKHHIPIKDMLTILESVS  CjFlbA
509 LLSYAEVQKLLKELPETQKKLVDDLIPGTVTATTVQRVLQSLLRERVSIRDLPQILEGVG  CcFlbF
512 FIGIQETRYLLEQMEGGYGELIKEVQR-IVPLQRMTEILQRLVGEDISIRNMRSILEAMV  YpLcrD
496 YFGIQETKHMLDQLEAKFPDLLKEVLRH-ATVQRISEVLQRLLSERVSVRNMKLIMEALA  StInvA
477 IFGIQETKNMLDQFENRYPDLLKEVFRHV-TIQRISEVLQRLLGENISVRNLKLIMESLA  SfMxiA
      .*   .*      .. .  .           .  .*. *. . .... .  *.*

595 DIAPLVQNDVNILTEQVRARLSRVITNAPKSEDGRLKFLTFSTDSEQFLLNKLRENGTSK  HpFlbA
588 DIAR-VSKSFDMIIEKVRASLARMITNMYLDDKGNLDIFILDSASSAVLMENVQFRDGSY  CjFlbA
569 EAAPHTA-SVTQLVEQVRARLARQLCWANRGDDGALPIITLSADWEQAFAEALIGPGDDK  CcFlbF
571 EWGQK-EKDVVQLTEYIRSSLKRYICYKYANGNNILPAYLFDQEVEEKIRSGVRQTSAGS  YpLcrD
555 LWAPR-EKDVINLVEHIRGAMARYICHKF-ANGGELRAVMVSAEVEDVIRKGIRQTSGST  StInvA
536 LWAPR-EKDVITLVEHVRASLSRYICSK-IAVSGEIKVVMLSGYIEDAIRKGIRQTSGGS  SfMxiA
     ..   ...  . * .*. . * ..       . .    .   .        .

655 SLLLNVGELQKLIFAVSEEAMKVLQKGIAPVILIVEPNLRKALSNQMEQARIDVIVLSHA  HpFlbA
647 HLPLSVAQTGTLVDTLRAEVAAVANGRIKPFILCVEPQLRKFIADICYNFSINIVVLSFA  CjFlbA
628 QLALPPSRLQDFIRGVRDSFERAALAGEAPVLL-TSPGVRPYVRSIIERFRGQTVVMSQN  CcFlbF
630 YLALEPAVTESLLEQVRKTIGDLSQIQSKP-VLIVSMDIRRYVRKLIESEYYGLPVLSYQ  YpLcrD
613 FLSLDPFASANLMDLITLKLDDLLIAH-KDLVLLTSVDVRRFIKKMIEGRFPDLEVLSFG  StInvA
594 FLNMDIEVSDEVMETLAHALREL-RNAKKNFVLLVSVDIRRFVKRLIDNRFKSILVISYA  SfMxiA
     *  .       .                    ..  * ..   *       ..       *.*

715 ELDPNSNFEALGTIHINF                                            HpFlbA
707 EIAENTNFNTEGIIRIEL                                            CjFlbA
687 EIHPRARLKTVGMV----                                           CcFlbF
689 ELTQQINIQPLGRICL--                                           YpLcrD
672 EIADSKSVNVIKTI----                                           StInvA
653 EIDEAYTINVLKTI----                                           SfMxiA
    *.          . .
```

FIG. 3D

Replacement Sheet

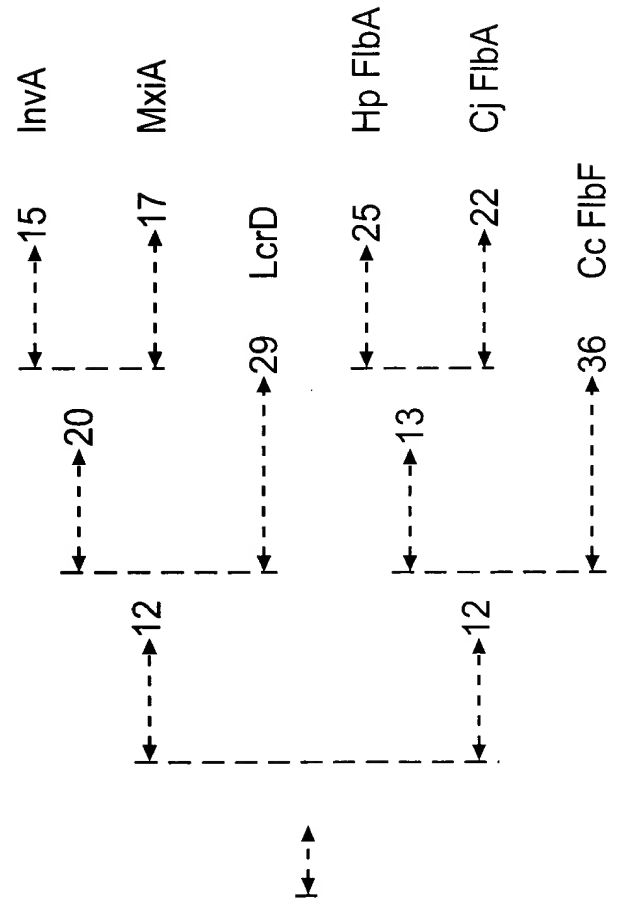


FIG. 4

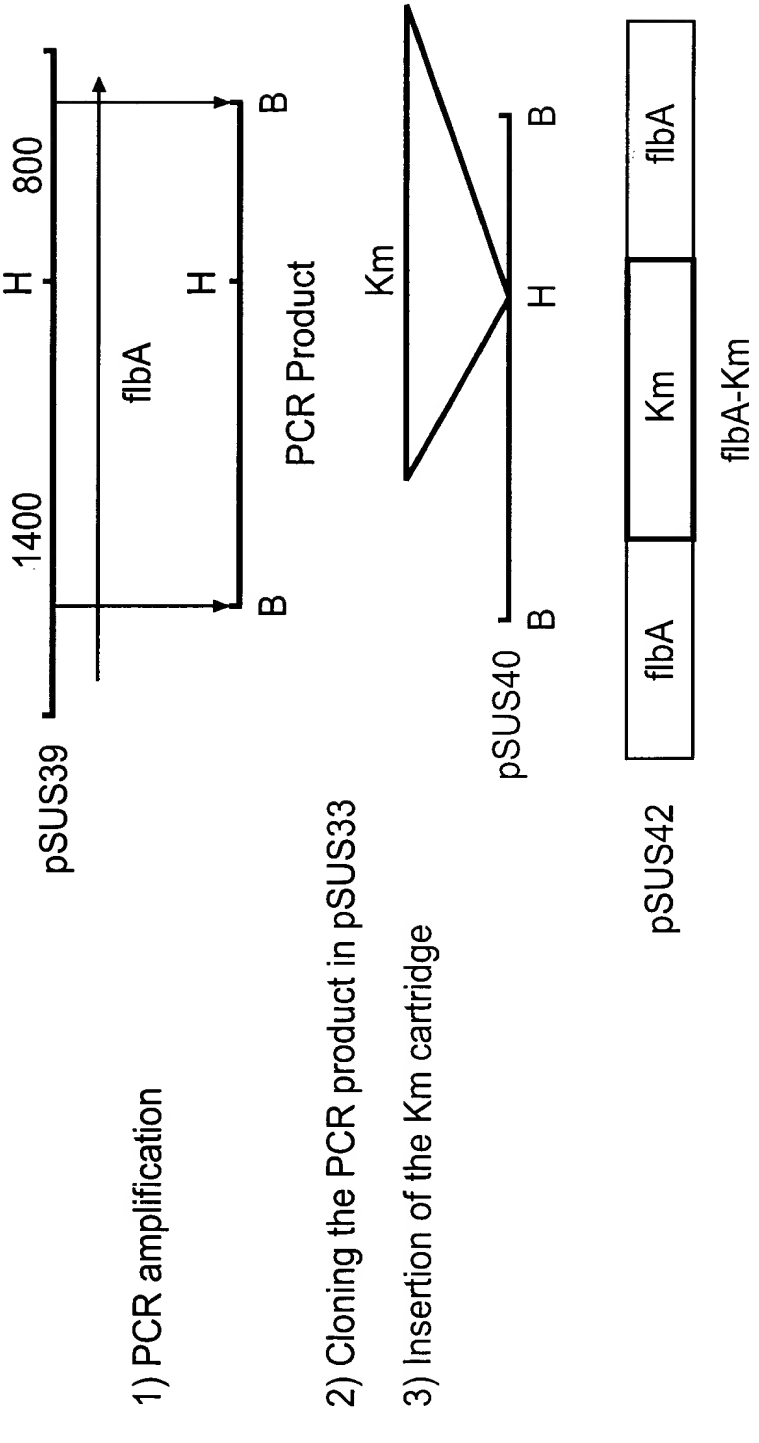


FIG. 5

Replacement Sheet

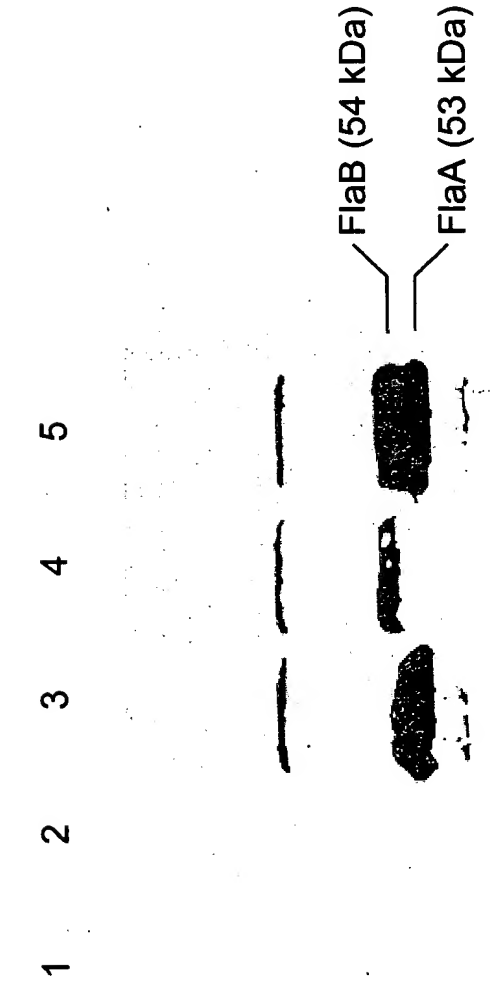


FIG. 6

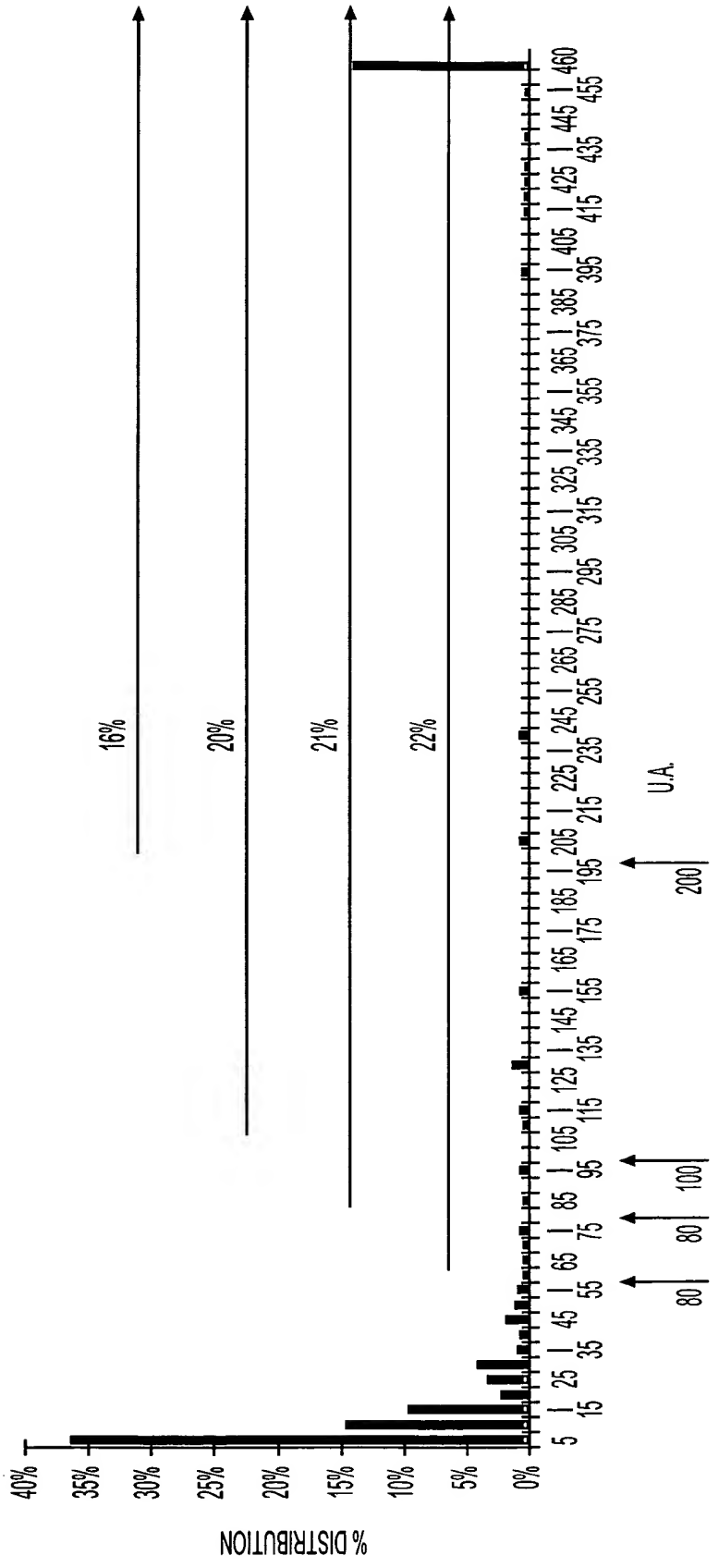


FIG. 7

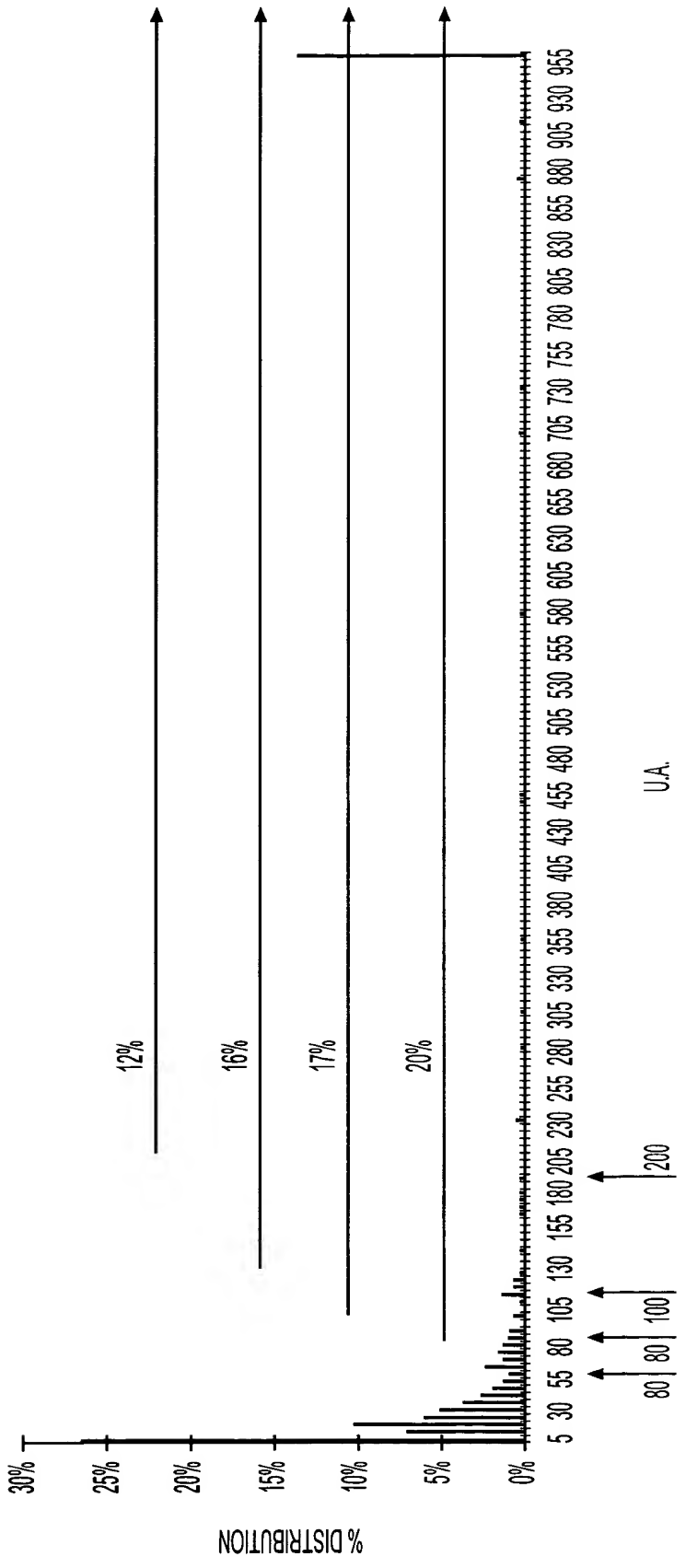


FIG. 8

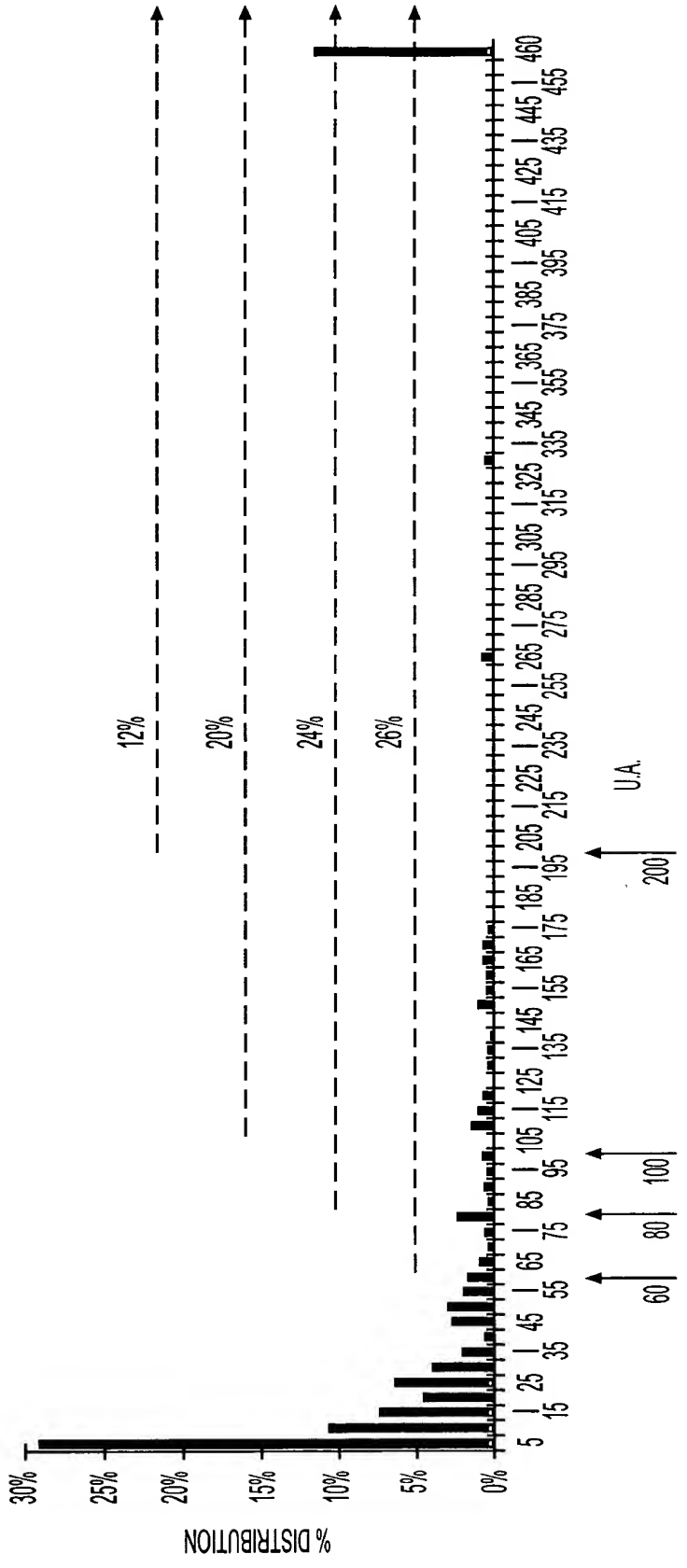


FIG. 9

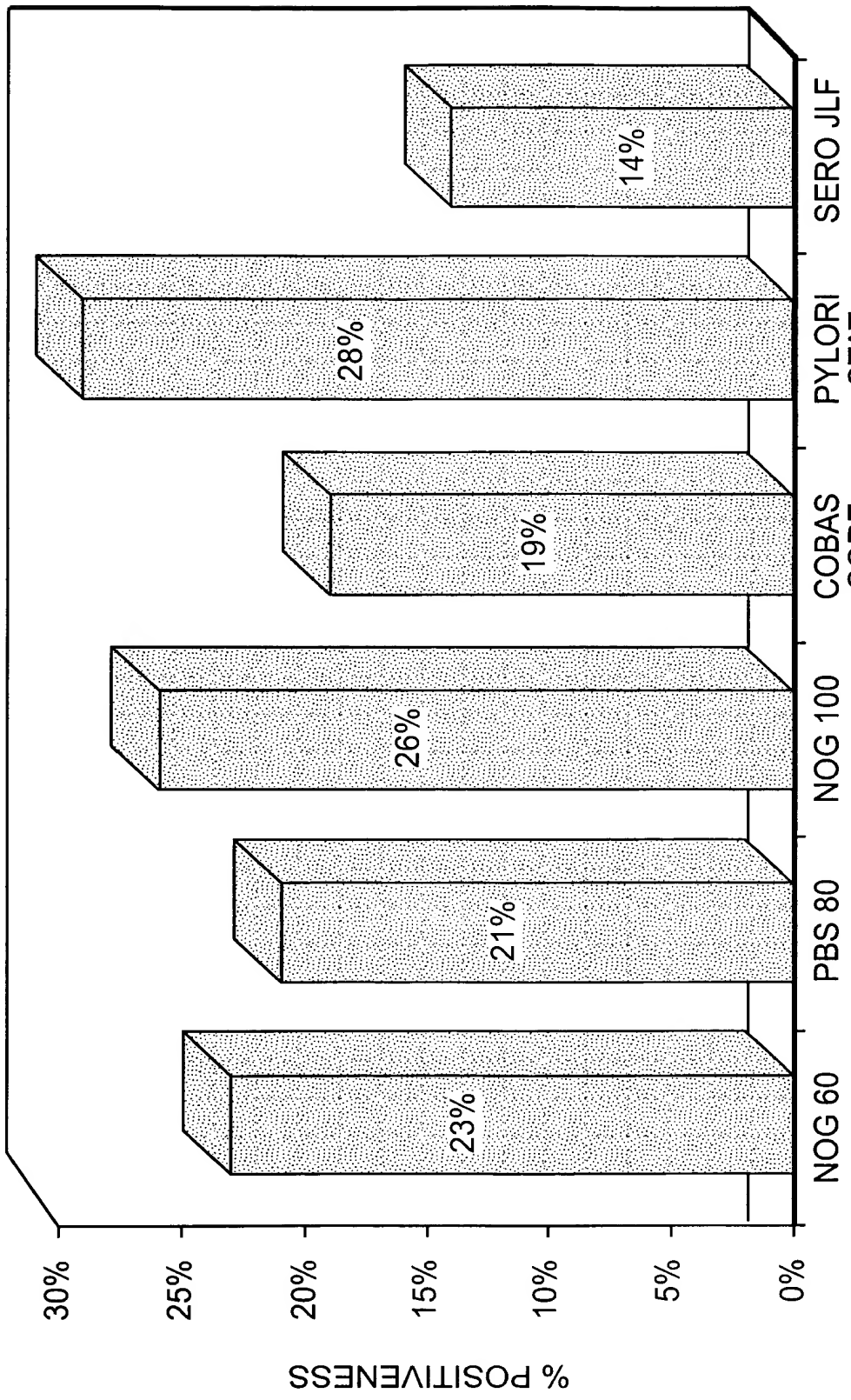


FIG. 10

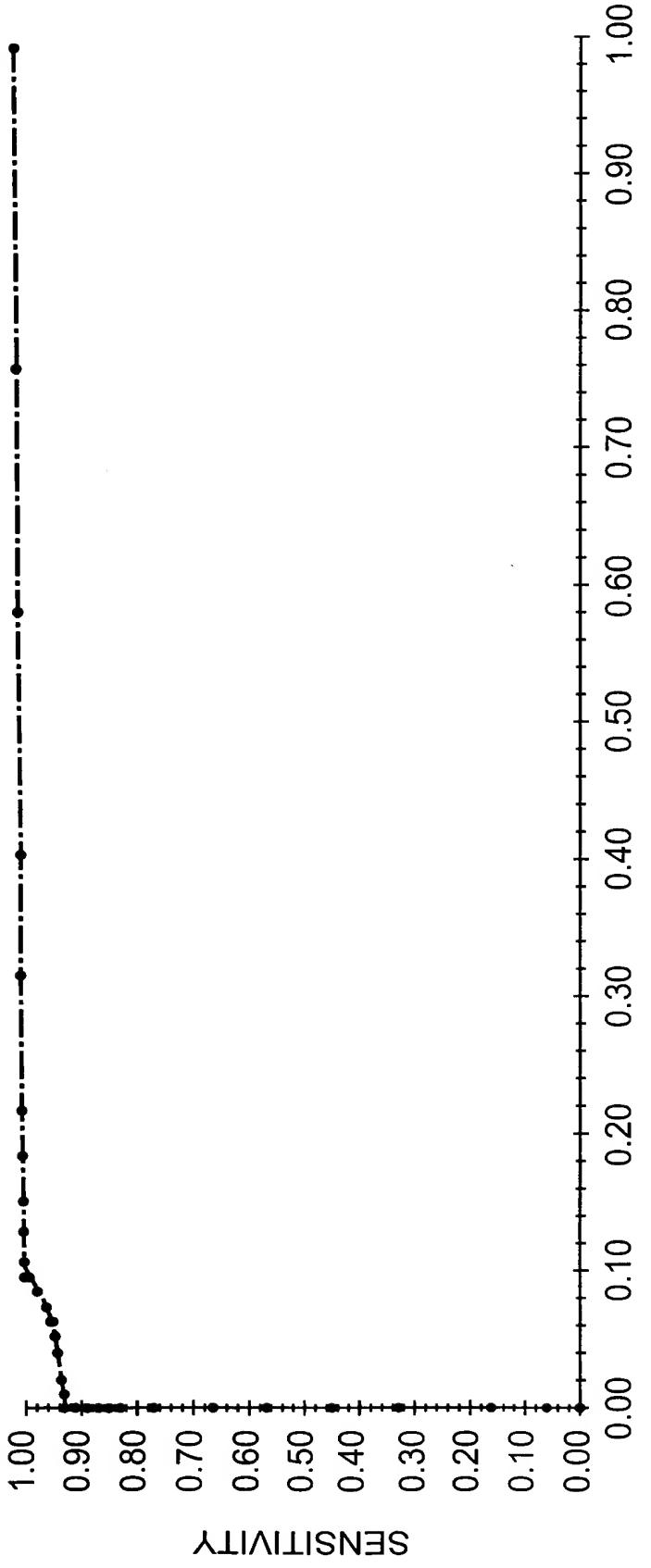
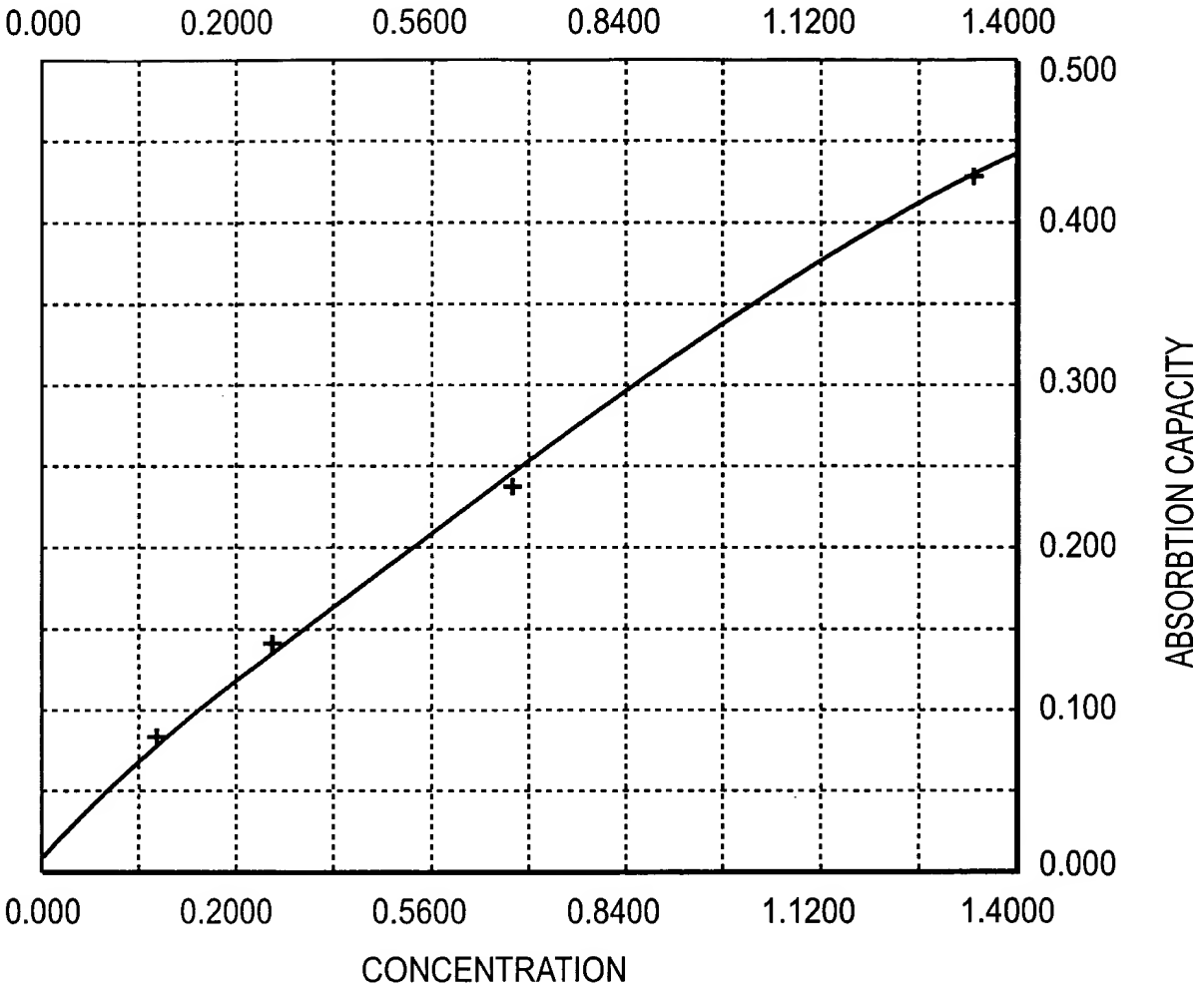


FIG. 11



TYPE OF EXTRACT	DO @ 750nm	CONCENTRATION IN mg/ml
GLYCINE (AFTER CENTRIFUGATION FOR 15 min @ 3000 g)	0.028	0.284
N-OCTYL-GLYCOSIDE	0.087	1.004
SUPERNATANT 1 (AFTER 1ST PBS WASHING)	0.059	0.844
SUPERNATANT 2 (AFTER 2nd PBS WASHING)	0.015	0.1105

FIG. 12

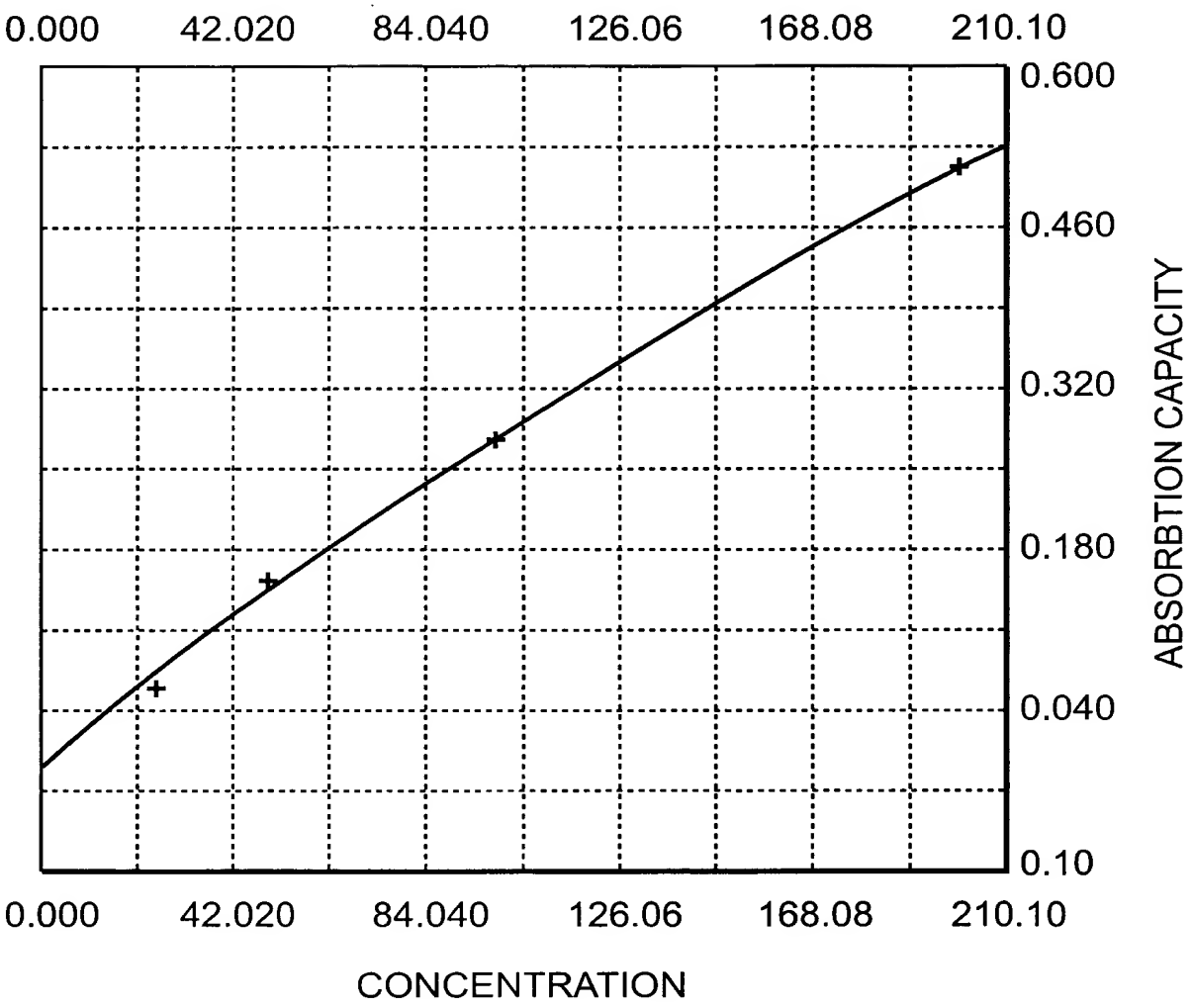


FIG. 13(A)

TYPE OF EXTRACT	DO @ 760 nm	CONCENTRATION IN µg/ml
GLYCINE (AFTER CENTRIFUGATION FOR 15min @ 3000g)	0.279	202.86
N-OCTYL-GLUCOSIDE	0.243	873.99
SUPERNATANT 1 (AFTER 1ST PBS WASHING)	0.361	539.2
SUPERNATANT 2 (AFTER 2ND PBS WASHING)	0.218	77.875

TYPE OF EXTRACT	DO @ 760 nm	CONCENTRATION IN µg/ml
GLYCINE RESIDUE (AFTER 15 min OF CENTRIFUGATION AT 3000g)	0.099	297.5
GLYCINE RESIDUE (AFTER EXTRACTION)	0.093	2778.7
N-OCTYL-GLUCOSIDE (AFTER EXTRACTION)	0.275	972.0

FIG. 13B

Replacement Sheet